

Amendments to the Specification:

Please replace the paragraph beginning at page 3, line 24 with the following amended paragraph:

-- The "percent identity" (or "percent homology") of two amino acid sequences or of two nucleic acids can be determined using the algorithm of Thompson et al. (CLUSTAL W, 1994 Nucleic Acids Res. 22: 4673-4680). An amino acid sequence or a nucleotide sequence can also be used as a "query sequence" to perform a search against public databases to, for example, identify related sequences. Such searches can be performed using the algorithm of Karlin and Altschul (1990 Proc. Natl. Acad. Sci. USA 87: 2264-2268), modified as in Karlin and Altschul (1993 Proc. Natl. Acad. Sci. USA 90: 5873-5877). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (1990 J. Mol. Biol. 215: 403-410). BLAST nucleotide searches are performed with the NBLAST program, score = 100, wordlength = 12. BLAST protein searches are performed with the XBLAST program, score = 50, wordlength = 3. Where gaps exist between two sequences, Gapped BLAST is utilized as described in Altschul et al. (1997 Nucleic Acids Res. 25: 3389-3402). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) are used. See [www.ncbi.nlm.nih.gov/](http://www.ncbi.nlm.nih.gov/)--

Please replace the three paragraphs beginning at page 16, line 29 with the following amended paragraphs:

-- *Transformation of plasmid DNAs into P. pastoris.* Plasmid DNA (10 µg) harboring the engineered lipase gene was digested with *EcoRV* in a total volume of 20 µL for 2 h. Linearized plasmid was transformed into *P. pastoris* by the electroporation method. High voltage pulses (1.5 kV) were delivered to 100 µL samples in 0.2 cm electrode gap cuvettes (Bio-Rad Laboratories) by using a GENE PULSER electroporation apparatus with the Pulse Controller (Bio-Rad Laboratories). Individual colonies of transformants were pitched and patched on tributyrin-emulsion YPD plates. The lipase-secreting transformants were identified by the clear

zone on the opaque tributyrin emulsion. *P. pastoris* transformed with pGAPZαC was used as a negative control.

*Purification of recombinant LIP2.* The culture medium from *P. pastoris* was concentrated by ultrafiltration on a 30,000 molecular weight cut-off membrane. These samples were then applied onto a HIPREP 16/10 Octyl FF chromatographic column (Pharmacia Biotech). The column was washed with 5 column volumes of TE buffer plus 1 mM CHAPS and then 4 mM CHAPS. Bound proteins were then eluted with 5 column volumes of TE buffer containing 30 mM CHAPS. The eluted materials were dialyzed against TE buffer.

The eluted proteins were then applied to a HIPREP 16/10 Q XL column (Pharmacia Biotech) equilibrated with TE buffer and the proteins were eluted using a linear gradient of 0 to 300 mM (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> over 5 column volumes. Protein concentrations in the fractions were measured with the Bio-Rad assay kit and esterase activity was determined using *p*-nitrophenyl butyrate as a substrate. Purified proteins were stored in a storage buffer (60 mM KCl, 10 mM Tris-HCl, 1.25 mM EDTA, 1% Triton X-100, and 17% glycerol, pH 7.5) at -20°C.--

Please replace the paragraph beginning at page 5, line 24 with the following amended paragraph:

-- Set forth below are the mutant nucleic acid sequences of *C. rugosa* lipase 2, *C. rugosa* lipase 3, *C. rugosa* lipase 4, *C. rugosa* lipase 5, and *C. rugosa* lipase 8, wherein all the CTG codons corresponding to serine in the wild-type DNA have been substituted with one of the six universal serine codons (i.e., TCT, TCC, TCA, TCG, AGT, or AGC). The mutated nucleotides are represented in black background. Also shown are the encoded amino acid sequences. The introduced N-terminal peptide (i.e., SMNSRGPAGRLGS) is underlined. Mutated amino acid residues are rendered in bold.

Mutant *C. rugosa* lipase 2

TCGATGAATTCACGTGGCCCAGCCGGCCGTCTCGGATCGGTACCCACCGCCACGCTCGCC 60

S M N S R G P A G R L G S V P T A T L A 20

AACGGCGACACCATCACCGGTCTCAACGCCATTGTCAACGAAAAGTTTCTCGGCATACCG 120  
N G D T I T G L N A I V N E K F L G I P 40  
TTTGGCCGAGCCGCCCCGTGGGCAGCCTCCGCTTCAAGCCGCCCCGTGCCGTACTCGGCGTCG 180  
F A E P P V G S L R F K P P V P Y S A S 60  
CTCAACGGCCAGCAGTTTACCCTCTTACGGCCCCGTCTTGCATGCAGATGAACCCTATGGGC 240  
L N G Q Q F T S Y G P S C M Q M N P M G 80  
TCGTTTGAGGACACACTTCCCAAGAATGCGCTTGACTTGGTGCTCCAGTCCAAGATCTTC 300  
S F E D T L P K N A L D L V L Q S K I F 100  
CAAGTGGTGCTTCCCAACGACGAGGACTGTCTCACCATCAACGTGATCCGGCCGCCCCGGC 360  
Q V V L P N D E D C L T I N V I R P P G 120  
ACCAGGGCCAGTGCTGGTCTCCCGGTGATGCTCTGGATCTTTGGCGGTGGGTTTGAGCTT 420  
T R A S A G L P V M L W I F G G G F E L 140  
GGCGGCTCCAGCCTCTTTCCAGGAGACCAGATGGTGGCCAAGAGCGTGCTCATGGGTAAA 480  
G G S S L F P G D Q M V A K S V L M G K 160  
CCGGTGATCCACGTGAGCATGAACTACCGCGTGGCGTCATGGGGGTTCTTGCCCGGCCCC 540  
P V I H V S M N Y R V A S W G F L A G P 180  
GACATCCAGAACGAAGGCAGCGGGAACGCCGGCTTGCATGACCAGCGCTTGGCCATGCAG 600  
D I Q N E G S G N A G L H D Q R L A M Q 200  
TGGGTGGCGGACAACATTGCTGGGTTTGGCGGCGACCCGAGCAAGGTGACCATATACGGC 660  
W V A D N I A G F G G D P S K V T I Y G 220  
GAGTCTGCGGGCAGCATGTCGACGTTTGTGCACCTTGTGTGGAACGACGGCGACAACACG 720  
E S A G S M S T F V H L V W N D G D N T 240  
TACAACGGCAAGCCGTTGTTCCGCGCCGCCATCATGCAGTCTGGCTGCATGGTGCCGTCT 780  
Y N G K P L F R A A I M Q S G C M V P S 260  
GACCCGGTGGACGGCACGTACGGCACCGAGATCTACAACCAGGTGGTGGCGTCTGCCGGG 840  
D P V D G T Y G T E I Y N Q V V A S A G 280

TGTGGCAGTGCCAGCGACAAGCTCGCGTGCTTGCGGGCCTT**TCT**CAGGACACGTTGTAC 900  
C G S A S D K L A C L R G L S Q D T L Y 300  
CAGGCCACGAGCGACACGCCCCGGCGTGTTGGCGTACCGCTCGTTGCGGTTG**TCT**TATCTC 960  
Q A T S D T P G V L A Y P S L R L S Y L 320  
CCGCGGCCCCGACGGCACCTTCATCACCGACGACATGTATGCCTTGCTGCGGGACGGCAAG 1020  
P R P D G T F I T D D M Y A L V R D G K 340  
TACGCACACGTGCCGGTGATCATCGGCGACCAGAACGACGAGGGCACTTTGTTTGGGCTC 1080  
Y A H V P V I I G D Q N D E G T L F G L 360  
**TCTTCT**TTGAACGTGACCACAGATGCTCAGGCACGGGCGTACTTCAAGCAG**TCT**TTCATC 1140  
S S L N V T T D A Q A R A Y F K Q S F I 380  
CACGCCAGCGATGCGGAGATCGACACGTTGATGGCGGGCTACACCAGCGACATCACCCAG 1200  
H A S D A E I D T L M A A Y T S D I T Q 400  
GGT**TCT**CCGTTCGACACCGGCATCTTCAATGCCATCACCCCGCAGTTCAAACGGATC**TCT** 1260  
G S P F D T G I F N A I T P Q F K R I S 420  
GCGTTGCTTGCGGACCTTGCGTTCACGCTTGCGCGTCGCTACTTCCTCAACTACTACCAG 1320  
A L L G D L A F T L A R R Y F L N Y Y Q 440  
GGCGGCACCAAGTACTCGTT**CTCT****TCT**AAGCAGCTT**TCT**GGGTTGCCCCGTCTTGGGCACC 1380  
G G T K Y S F L S K Q L S G L P V L G T 460  
TTCCACGGCAACGACATCATCTGGCAGGACTACTTGGTGGGCAGCGGCAGTGTGATCTAC 1440  
F H G N D I I W Q D Y L V G S G S V I Y 480  
AAACACGCGTTCATTGCGTTTGCCAACGACCTCGACCCGAACAAGGCGGGCTTGTGGACC 1500  
N N A F I A F A N D L D P N K A G L W T 500  
AACTGGCCACGTACACCAGCAG**CTCT**CAG**TCT**GGCAACAACCTTGATGCAGATCAACGGC 1560  
N W P T Y T S S S Q S G N N L M Q I N G 520  
TTGGGGTTGTACACCGGCAAGGACAACCTTCCGCCCCGGATGCGTACAGCGCCCTCTTTTCC 1620  
L G L Y T G K D N F R P D A Y S A L F S 540

AACCCGCC**GTCT**TTCTTTGTG (SEQ ID NO:1) 1641

N P P S F F V (SEQ ID NO:2) 547

Mutant *C. rugosa* lipase 3

**TCGATGAATTACGTGGCCCAGCCGGCCGTCTCGGATCGGTA**CCCACCGCCAAGCTCGCC 60  
S M N S R G P A G R L G S V P T A K L A 20  
AACGGCGACACCATCACCGGTCTCAACGCCATCATCAACGAGGCGTTCCTCGGCATTCCC 120  
N G D T I T G L N A I I N E A F L G I P 40  
TTTGCCGAGCCGCCGGTGGGCAACCTCCGCTTCAAGGACCCTGTGCCGTACTCTGGCTCG 180  
F A E P P V G N L R F K D P V P Y S G S 60  
CTCAACGGCCAGAAGTT**CACTTCT**TACGGCCCG**TCT**TGCATGCAGCAGAACCCCCGAGGGC 240  
L N G Q K F T S Y G P S C M Q Q N P E G 80  
ACGTTTGAAGAGAACCTTGGCAAGACGGCACTCGACTTGGTGATGCAGTCCAAGGTGTTC 300  
T F E E N L G K T A L D L V M Q S K V F 100  
CAGGCGGTGCTTCCCCAGAGTGAGGACTGCCTCACCATCAACGTGGTGCGGCCGCCGGGC 360  
Q A V L P Q S E D C L T I N V V R P P G 120  
ACCAAGGCGGGCGCCAACCTCCCGGTATGCTCTGGATCTTTGGCGGTGGGTTTGAGATC 420  
T K A G A N L P V M L W I F G G G F E I 140  
GGCAGCCCCACCATCTTCCCTCCCGCCCAGATGGTCACCAAGAGTGTGCTCATGGGCAAG 480  
G S P T I F P P A Q M V T K S V L M G K 160  
**CA**CATCATCCACGTGGCCGTCAACTACCGTGTTGCCTCGTGGGGGTCTTGGCTGGTGAT 540  
H I I H V A V N Y R V A S W G F L A G D 180  
GACATCAAGGCCGAGGGCAGCGGGAACGCCGGCTTGAAGGACCAGCGTTTGGGCATGCAG 600  
D I K A E G S G N A G L K D Q R L G M Q 200  
TGGGTGGCAGACAACATTGCCGGGTTCGGCGGCGACCCGAGCAAGGTGAC**T**ATCTTTGGC 660

W V A D N I A G F G G D P S K V T I F G 220  
GAGTCTGCGGGCAGCATGTCCGTGTTGTGCCACCTCATCTGGAACGACGGCGACAACACG 720  
E S A G S M S V L C H L I W N D G D N T 240  
TACAAGGGCAAGCCGTTGTTCCGCGCGGGCATCATGCAGTCTGGAGCCATGGTGCCGTCT 780  
Y K G K P L F R A G I M Q S G A M V P S 260  
GACCCGGTGGACGGCAGTACGGCAACGAGATCTACGACCTCTTTGTCTCGAGTGCTGGC 840  
D P V D G T Y G N E I Y D L F V S S A G 280  
TGTGGCAGCGCCAGCGACAAGCTCGCGTGCTTGCGCAGTGCGTCTAGCGACACCTTGCTC 900  
C G S A S D K L A C L R S A S S D T L L 300  
GATGCCACCAACAACACTCCTGGGTTCTTGGCGTACTCCTCGTTGCGGTTGTCTTATCTC 960  
D A T N N T P G F L A Y S S L R L S Y L 320  
CCGCGGCCCCGACGGCAAGAACATCACCGATGACATGTACAAGTTGGTGCGCGACGGCAAG 1020  
P R P D G K N I T D D M Y K L V R D G K 340  
TATGCAAGCGTTCCCGTGATCATTGGCGACCAGAACGACGAGGGCACCATCTTTGGGCTC 1080  
Y A S V P V I I G D Q N D E G T I F G L 360  
TCTTCTTTGAACGTGACCACGAATGCTCAGGCCCGTGCTTACTTCAAGCAGTCTTTCATC 1140  
S S L N V T T N A Q A R A Y F K Q S F I 380  
CACGCCAGCGACGCGGAGATCGACACCTTGATGGCGGCGTACCCCCAGGACATCACCCAG 1200  
H A S D A E I D T L M A A Y P Q D I T Q 400  
GGTTCTCCGTTCGACACGGGTGTTCTCAACGCCCTACCCCGCAGTTCAAGAGAATCTCT 1260  
G S P F D T G V L N A L T P Q F K R I S 420  
GCGGTGCTCGGCGACCTTGCAATTCATCCACGCCCCGCGCTACTTCTCAACCACTTCCAG 1320  
A V L G D L A F I H A R R Y F L N H F Q 440  
GGCGGCACCAAGTACTCGTTCCTCTCTAAGCAGCTCTCTGGGTTGCCAATCATGGGCACC 1380  
G G T K Y S F L S K Q L S G L P I M G T 460  
TTCCATGCCAACGACATTGTGTGGCAGGACTACTTGTGGGAAGCGGCAGCGTCATCTAC 1440

F H A N D I V W Q D Y L L G S G S V I Y 480  
AACAACGCGTTTATCGCGTTCGCCACCGACTTGGACCCCAACACCGCGGGGTGTTGGTG 1500  
N N A F I A F A T D L D P N T A G L L V 500  
AACTGGCCCAAGTACACCAGCAGCTCTCAGTCTGGCAACAACCTTGATGATGATCAACGCC 1560  
N W P K Y T S S S Q S G N N L M M I N A 520  
TTGGGCTTGTACACCGCAAGGACAACCTCCGCACCGCTGGCTACGACGCGTTGATGACC 1620  
L G L Y T G K D N F R T A G Y D A L M T 540  
AACCCGTCTTTCTTTCTTTGTG (SEQ ID NO:3) 1641  
N P S S F F V (SEQ ID NO:4) 547

Mutant *C. rugosa* lipase 4

TCGATGAATTACAGTGGCCCGCCGCGCTCTCGGATCGGTACCCACTGCCACGCTCGCC 60  
S M N S R G P A G R L G S V P T A T L A 20  
AACGGCGACACCATCACCGGTCTCAACGCCATCATCAACGAGGCGTTCCTCGGTATTCCC 120  
N G D T I T G L N A I I N E A F L G I P 40  
TTTGCTCAGCCGCCGGTGGGCAACCTCCGCTTCAAGCCGCCTGTGCCGTACTCGGCGTCT 180  
F A Q P P V G N L R F K P P V P Y S A S 60  
CTCAATGGTCAGAAGTTTACTTCGTATGGCCCTTCGTGCATGCAGATGAACCCATTGGGC 240  
L N G Q K F T S Y G P S C M Q M N P L G 80  
AACTGGGACTCCTCGCTTCCCAAGGCTGCCATCAACTCCCTTGATGCAGTCCAAGCTCTTC 300  
N W D S S L P K A A I N S L M Q S K L F 100  
CAGGCGGTGCTTCCTAACGGCGAGGACTGTCTCACCATCAACGTGGTGCGGCCGTCAGGC 360  
Q A V L P N G E D C L T I N V V R P S G 120  
ACCAAGCCGGGTGCCAACCTCCCCGTGATGGTGTGGATTTTTGGCGGCGGGTTTGAGGTT 420  
T K P G A N L P V M V W I F G G G F E V 140  
GGCGGCTCCAGTCTCTTCCCTCCCGCACAGATGATCACCGCCAGCGTGCTTATGGGCAAG 480

G G S S L F P P A Q M I T A S V L M G K 160  
CCCATCATCCACGTGAGCATGAACTACCGCGTTGCTTCGTGGGGGTTCTTGGCTGGTCCA 540  
P I I H V S M N Y R V A S W G F L A G P 180  
GACATCAAGGCCGAGGGCAGCGGGAACGCCGTTTGCACGACCAACGCTTGGGTTTGCAG 600  
D I K A E G S G N A G L H D Q R L G L Q 200  
TGGGTGGCGGACAACATTGCCGGGTTTCGGCGGCGACCCGTCCAAGGTGACCATCTTTGGT 660  
W V A D N I A G F G G D P S K V T I F G 220  
GAGTCGGCGGGCAGCATGTCCGTAATGTGTCAGCTCCTCTGGAACGACGGCGACAACACG 720  
E S A G S M S V M C Q L L W N D G D N T 240  
TACAACGGCAAGCCGTTGTTCCGTGCCGCCATCATGCAGTCTGGGGCCATGGTGCCGTG 780  
Y N G K P L F R A A I M Q S G A M V P S 260  
GACCCGGTGGATGGGCCCTACGGCACGCAGATCTACGACCAGGTGGTTGCTTCAGCCGGC 840  
D P V D G P Y G T Q I Y D Q V V A S A G 280  
TGTGGCAGTGCCAGCGACAAGCTCGCGTGCTTGCGCAGCATCTCGAACGACAAACTCTTC 900  
C G S A S D K L A C L R S I S N D K L F 300  
CAGGCCACCAGCGACACTCCGGGGGCCTTGGCGTACCCCTCGTTGCGGTTGCTGTTTCTC 960  
Q A T S D T P G A L A Y P S L R L S F L 320  
CCGCGGCCCCGACGGCACCTTCATCACCGATGACATGTTCAAGTTGGTGCGCGACGGCAAG 1020  
P R P D G T F I T D D M F K L V R D G K 340  
TGTGCCAACGTTCCGGTGATCATTGGCGACCAGAACGACGAGGGCACAGTGTTCGCTTG 1080  
C A N V P V I I G D Q N D E G T V F A L 360  
TCCAGGTTGAACGTGACTACGGATGCTCAGGCACGCCAGTACTTCAAGGAAAGCTTCATC 1140  
S S L N V T T D A Q A R Q Y F K E S F I 380  
CACGCCAGCGACGCGGAGATCGACACCTTGATGGCGGCGTACCCAGCGACATCACCCAG 1200  
H A S D A E I D T L M A A Y P S D I T Q 400  
GGTAGTCCGTTTCGACACCGGCATCTTCAACGCCATCACCCCGCAGTTCAAACGGATTGCA 1260



G S P F D T G I F N A I T P Q F K R I A 420  
GCGGTGCTTGGTGACCTTGCGTTCACCTCTCCCCGGCGCTACTTCCTCAACCACTTCCAG 1320  
A V L G D L A F T L P R R Y F L N H F Q 440  
GGCGGCACCAAGTACTCGTTCCTCTCGAAGCAGCTTAGTGGGTTGCCGGTGATTGGCACC 1380  
G G T K Y S F L S K Q L S G L P V I G T 460  
CACCACGCCAACGACATTGTGTGGCAGGACTTTTGGTGAGCCACAGCAGCGCCGTGTAC 1440  
H H A N D I V W Q D F L V S H S S A V Y 480  
AACACGCGTTTATTGCCTTTGCCAACGACCTCGACCCGAACAAGGCCGTTTGCTTGTG 1500  
N N A F I A F A N D L D P N K A G L L V 500  
AACTGGCCCAAGTACACCAGCAGCTCTCAGTCAGGCAACAACCTGTTGCAGATCAACGCC 1560  
N W P K Y T S S S Q S G N N L L Q I N A 520  
TTGGGCTTGTACACCGGCAAGGACAACCTCCGCACCGCTGGCTACGACGCGTTGTTTACC 1620  
L G L Y T G K D N F R T A G Y D A L F T 540  
AACCCGTCTTCTTTCTTTGTG (SEQ ID NO:5) 1641  
N P S S F F V (SEQ ID NO:6) 547

Mutant *C. rugosa* lipase 5

TCGATGAATTACGTGGCCCAGCCGGCCGTCTCGGATCGGTACCACAGCCACGCTCGCC 60  
S M N S R G P A G R L G S V P T A T L A 20  
AACGGCGACACCATCACCGGTCTCAACGCCATCATCAACGAGGCGTTCCTCGGCATTCCC 120  
N G D T I T G L N A I I N E A F L G I P 40  
TTTGCCGAGCCGCCGGTGGGCAACCTCCGCTTCAAGGACCCTGTGCCGTACCGTGGGTCT 180  
F A E P P V G N L R F K D P V P Y R G S 60  
CTCAACGGTCAATCCTTCACCGCGTACGGTCCGTCTTGCATGCAGCAGAACCCCGAGGGC 240  
L N G Q S F T A Y G P S C M Q Q N P E G 80  
ACCTACGAGGAGAACCTCCCCAAGGTGGCGCTTGACTTGGTGATGCAGTCCAAGGTGTTT 300

T Y E E N L P K V A L D L V M Q S K V F 100  
CAGGCTGTTCTCCCCAACAGCGAGGACTGCCTCACCATCAACGTGGTGCGGCCGCCGGGC 360  
Q A V L P N S E D C L T I N V V R P P G 120  
ACCAAGGCGGGCGCCAACCTCCCGGTCATGCTCTGGATCTTTGGCGGTGGGTTTGAGATC 420  
T K A G A N L P V M L W I F G G G F E I 140  
GGCAGCCCCACCATCTTCCCTCCCGCTCAGATGGTCTCCAAGAGTGTGCTCATGGGCAG 480  
G S P T I F P P A Q M V S K S V L M G E 160  
CCCATCATCCACGTGGCCGTCAACTACCGCTTGGCGTCCTTTGGTTTCTTGGCCGGTCCG 540  
P I I H V A V N Y R L A S F G F L A G P 180  
GACATCAAGGCCGAGGGCAGCTCCAATGCCGGCCTCAAGGACCAGCGCTTGGGCATGCAG 600  
D I K A E G S S N A G L K D Q R L G M Q 200  
TGGGTGGCAGACAACATTGCCGGGTTCGGCGGCGACCCGAGCAAGGTGACCATCTTTGGC 660  
W V A D N I A G F G G D P S K V T I F G 220  
GAGTCTGCGGGCAGCATGTCCGTGTTGTGCCACCTTCTCTGGAATGGCGGCGACAACACG 720  
E S A G S M S V L C H L L W N G G D N T 240  
TACAAGGGCAAGCCGTTGTTCCGCGCGGGCATCATGCAGTCTGGAGCCATGGTGCCGTCT 780  
Y K G K P L F R A G I M Q S G A M V P S 260  
GACCCGGTGGACGGCACCTATGGAACCCAAATCTATGACACGTTGGTGGCTTCTACGGGC 840  
D P V D G T Y G A Q I Y D T L V A S T G 280  
TGCAGCAGTGCCAGCAACAAGCTTGCGTGCTTGCGTGGTCTTCTACTCAGGCATTGCTC 900  
C S S A S N K L A C L R G L S T Q A L L 300  
GATGCCACCAACGACACCCCTGGGTCTTGTGCTACACCTCGTTGCGGTTGTCTATCTC 960  
D A T N D T P G F L S Y T S L R L S Y L 320  
CCGCGGCCCGACGGCGCCAACATCACCGATGACATGTACAAGTTGGTACGCGACGGCAAG 1020  
P R P D G A N I T D D M Y K L V R D G K 340  
TATGCAAGCGTTCCCGTGATCATTTGGCGACCAGAACGACGAGGGCTTCTTGTTGATCTC 1080

Y A S V P V I I G D Q N D E G F L F D L 360  
TCTTCTTTGAACACCACCACCGAGGCCGACGCCGAGGCATACCTCAGAAAGTCTTTCATC 1140  
S S L N T T T E A D A E A Y L R K S F I 380  
CACGCCACCGACGCCGATATCACCGCATTGAAGGCGGCGTACCCACGCGATGTCACCCAG 1200  
H A T D A D I T A L K A A Y P S D V T Q 400  
GGTTCTCCGTTTCGACACGGGCATTCTCAACGCCCTTACACCCAGCTCAAGCGGATCAAT 1260  
G S P F D T G I L N A L T P Q L K R I N 420  
GCTGTGCTTGGCGACCTCACCTTTACCCTCTCGCGCCGCTACTTCCTCAACCACTACACC 1320  
A V L G D L T F T L S R R Y F L N H Y T 440  
GGTGGTCCCAAGTACTCGTTCCTCTCTAAGCAGCTTTCTGGGTTGCCATTCTCGGTACG 1380  
G G P K Y S F L S K Q L S G L P I L G T 460  
TTCCACGCGAACGACATTGTGTGGCAGCACTTTTTGTTGGGCAGCGGCAGCGTCATCTAC 1440  
F H A N D I V W Q H F L L G S G S V I Y 480  
AACAACGCGTTTCATCGCGTTTGCCACCGACTTGGAACCCCAACACCGCGGGCTTGCTGTG 1500  
N N A F I A F A T D L D P N T A G L S V 500  
CAGTGGCCCAAGTACACCAGCAGCTCTCAGGCGGGGGACAACCTTGATGCAGATCAGTGCC 1560  
Q W P K Y T S S S Q A G D N L M Q I S A 520  
TTGGGCTTGTTACACCGGCAAGGACAACCTCCGCACCGCCGGCTACAACGCTTTGTTTGCC 1620  
L G L Y T G K D N F R T A G Y N A L F A 540  
GACCCGTCTCACTTTTTTCGTG (SEQ ID NO:7) 1641  
D P S H F F V (SEQ ID NO:8) 547

Mutant *C. rugosa* lipase 8

TCGATGAATTCACGTGGCCCGAGCCGGCCGTCTCGGATCGGTACCCACTGCCACGCTCGCC 60  
S M N S R G P A G R L G S V P T A T L A 20  
AACGGCGACACCATCACCGGTCTCAACGCCATCATCAACGAGGCGTTCCCTCGGCATTCCC 120  
N G D T I T G L N A I I N E A F L G I P 40

TTTGCCGAGCCGCCGGTGGGCAACCTCCGCTTCAAGGACCCCGTGCCGTA CTCCGGCTCG 180  
F A E P P V G N L R F K D P V P Y S G S 60  
CTCGATGGCCAGAAGTTCACTTCTTACGGCCCGTCTTGCATGCAGCAGAACCCCGAGGGC 240  
L D G Q K F T S Y G P S C M Q Q N P E G 80  
ACCTACGAGGAGAACCTCCCCAAGGCAGCGCTCGACTTGGTGATGCAGTCCAAGGTGTTT 300  
T Y E E N L P K A A L D L V M Q S K V F 100  
GAGGCGGTGTCTCCGTCTAGCGAGGACTGTCTCACCATCAACGTGGTGCGGCCGCCGGGC 360  
E A V S P S S E D C L T I N V V R P P G 120  
ACCAAGGCGGGTGCCAACCTCCCGGTGATGCTCTGGATCTTTGGCGGCGGGTTTGAGGTG 420  
T K A G A N L P V M L W I F G G G F E V 140  
GGTGGCACCAGCACCTTCCCTCCCGCCCAGATGATCACCAAGAGCATTGCCATGGGCAAG 480  
G G T S T F P P A Q M I T K S I A M G K 160  
CCCATCATCCACGTGAGCGTCAACTACCGCGTGTCTGTCGTGGGGGTTCTTGCTGGCGAC 540  
P I I H V S V N Y R V S S W G F L A G D 180  
GAGATCAAGGCCGAGGGCAGTGCCAACGCCGTTTGAAGGACCAGCGCATGGGCATGCAG 600  
E I K A E G S A N A G L K D Q R M G M Q 200  
TGGGTGGCGGACAACATTGCGGCGTTTGGCGGCGACCCGACCAAGGTGACCATCTTTGGC 660  
W V A D N I A A F G G D P T K V T I F G 220  
GAGTCTGCGGGCAGCATGTCTGGTCATGTGCCACATTCTCTGGAACGACGGCGACAACACG 720  
E S A G S M S V M C H I L W N D G D N T 240  
TACAAGGGCAAGCCGCTCTTCCGCGCGGGCATCATGCAGTCTGGGGCCATGGTACCGTCG 780  
Y K G K P L F R A G I M Q S G A M V P S 260  
GACGCGTGGACGGCTCTACGGCAACGAGATCTTTGACCTCTTGGCGTCGACGCGGGC 840  
D A V D G V Y G N E I F D L L A S D A G 280  
TGCGGCAGCGCCAGCGACAAGCTTGCGTGCTTGCGCGGTGTGTCTAGCGACACGTTGGAG 900  
C G S A S D K L A C L R G V S S D T L E 300

GACGCCACCAACAACACCCCTGGGTTCTTGGCGTACTCCTCGTTGCGGTTG**TCTTAT**CTC 960  
D A T N. N T P G F L A Y S S L R L S Y L 320  
CC**G**CGGCCCCGACGGCGTGAACATCACCGACGACATGT**TT**GCCTTGGT**C**CGCGAGGGCAAG 1020  
P R P D G V N I T D D M **F** A L V R E G K 340  
TATGCA**AAGCGT****T**CCTGTGATCATCGGCGACCAGAACGACGAGGGCACCTTCTTTGGCACC 1080  
Y A **S** V P V I I G D Q N D E G T F F G T 360  
**TCTTTCT**TTGAACGTGACCACGGATGCC**G**AGGCCCGC**C**AGTACTTCA**G**CGAG**TCT**TTTGTC 1140  
S S L N V T T D A **E** A R **Q** Y F **T** Q S F V 380  
CACGCCAGCGACGCGGAG**C**TCGACACGTTGATGACGGCGTACCC**CAG**GACATCACCCAG 1200  
H A S D A E **L** D T L M T A Y P **Q** D I T Q 400  
GG**TTCT**CCGTTCGACACGGGT**G**TTCTCAACGCCCTCACCCCGCAGTTCAAGAGAAT**TCT** 1260  
G S P F D T G **V** L N A L T P Q F K R I S 420  
GCGGTGCTCGGCGACCTTG**C**CTT**CATCCACGC****C**CGTCGCTACTTCTCAACCACTACACC 1320  
A V L G D L **A** F **I** H A R R Y F L N H Y T 440  
GGCGGCACCAAGTACTCATTCTCT**TCT**AAGCAGCT**TCT**GGCTTGCCGGTGCTCGGAACG 1380  
G G T K Y S F L S K Q L S G L P V L G T 460  
TTCCACTCCAACGACATTGTCTTCCAGGACTACTTGTTGGGCAGCGGCTCGCTCATCTAC 1440  
F H S N D I V F Q D Y L L G S G S L I Y 480  
AACAACGCGTTCATTGCGTTTGCCACGGA**CT**TGGACCCCAACACCGCGGGTGTGGTG 1500  
N N A F I A F A T D L D P N T A G L L V 500  
AAGTGGCCCCGAGTACACCAGCAGCT**TCT**CAG**TCT**GGCAACA**CT**TGATGATGATCAACGCC 1560  
K W P E Y T S S S Q S G N N L M M I N A 520  
TTGGGCTTG**T**TACACCGCAAGGACA**CT****C**CGCACCGCGGCTACGACGCGTTGTTCTCC 1620  
L G L Y T G K D N **S** R T A G Y D A L F S 540  
AACCCGCGG**TCT**TTCTTTGTG (SEQ ID NO:9) 1641  
N P P S F F V (SEQ ID NO:10) 547 --

Please replace the paragraph beginning at page 14, line 4 with the following amended paragraph:

-- The polypeptide having the amino acid sequence of SEQ ID NO:2 differs from the wild-type *C. rugosa* lipase 2 by a N-terminal peptide (i.e., SMNSRGPAGRLGS) and 4 amino acids (i.e., A14V; T48S; R91L; H92D). The polypeptide having the amino acid sequence of SEQ ID NO:4 differs from the wild-type *C. rugosa* lipase 3 by the N-terminal peptide and 5 amino acids (i.e., A14V; P161H; I408V; F409L; I412L). The polypeptide having the amino acid sequence of SEQ ID NO:6 differs from the wild-type *C. rugosa* lipase 4 by the N-terminal peptide and 1 amino acid (i.e., A14V). The polypeptide having the amino acid sequence of SEQ ID NO:8 differs from the wild-type *C. rugosa* lipase 5 by the N-terminal peptide and 5 amino acids (i.e., A14V; K160E; T269A; G359D; S505Y). The polypeptide having the amino acid sequence of SEQ ID NO:10 differs from the wild-type *C. rugosa* lipase 1 by the N-terminal peptide and 17 amino acids (i.e., A14V; L197M; I266V; N278D; Y333F; N343S; I344V; Q370E; E373Q; K376T; I387L; G396Q; I408V; G427A; T429I; L430H; F530S).--